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OIKE

#2

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/021,121

DATE: 02/01/2002
 TIME: 11:33:53

Input Set : N:\Crf3\RULE60\10021121.raw
 Output Set: N:\CRF3\02012002\J021121.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Caras, Ingrid W
- 7 (ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor
- 9 (iii) NUMBER OF SEQUENCES: 10
- 11 (iv) CORRESPONDENCE ADDRESS:
 - 12 (A) ADDRESSEE: Genentech, Inc.
 - 13 (B) STREET: 1 DNA Way
 - 14 (C) CITY: South San Francisco
 - 15 (D) STATE: California
 - 16 (E) COUNTRY: USA
 - 17 (F) ZIP: 94080
- 19 (v) COMPUTER READABLE FORM:
 - 20 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - 21 (B) COMPUTER: IBM PC compatible
 - 22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - 23 (D) SOFTWARE: WinPatin (Genentech)
- 25 (vi) CURRENT APPLICATION DATA:
 - C--> 26 (A) APPLICATION NUMBER: US/10/021,121
 - C--> 27 (B) FILING DATE: 06-Dec-2001
 - 28 (C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
 - 31 (A) APPLICATION NUMBER: US/08/635,130
 - 32 (B) FILING DATE: 19-Mar-1996
- 35 (viii) ATTORNEY/AGENT INFORMATION:
 - 36 (A) NAME: Torchia, PhD., Timothy E.
 - 37 (B) REGISTRATION NUMBER: 36,700
 - 38 (C) REFERENCE/DOCKET NUMBER: P1001
- 40 (ix) TELECOMMUNICATION INFORMATION:
 - 41 (A) TELEPHONE: 650/225-8674
 - 42 (B) TELEFAX: 650/952-9881

ENTERED

43 (2) INFORMATION FOR SEQ ID NO: 1:

- 45 (i) SEQUENCE CHARACTERISTICS:
 - 46 (A) LENGTH: 1877 base pairs
 - 47 (B) TYPE: Nucleic Acid
 - 48 (C) STRANDEDNESS: Double
 - 49 (D) TOPOLOGY: Linear
- 51 (ix) FEATURE:
 - 52 (A) NAME/KEY: Extra Cellular Domain
 - 53 (B) LOCATION: 244-899
 - 54 (C) IDENTIFICATION METHOD:
 - 55 (D) OTHER INFORMATION:
- 57 (ix) FEATURE:

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58      (A) NAME/KEY: Transmembrane Domain
59      (B) LOCATION: 901-978
60      (C) IDENTIFICATION METHOD:
61      (D) OTHER INFORMATION:
63      (ix) FEATURE:
64      (A) NAME/KEY: signal peptide
65      (B) LOCATION: 244-321
66      (C) IDENTIFICATION METHOD:
67      (D) OTHER INFORMATION:
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72      GNTCTAGAA  TAGTGGATCC  CCCCAGGCTG  CAGGAATTCC  GACGGCCCCT  50
74      GGAAGGGCTC  TGGTGGGGCT  GAGCGCTCTG  CCGCGGGGGC  GCGGGCACAG  100
76      CAGGAAGCAG  GTCCGCGTGG  GCGCTGGGGG  CATCAGCTAC  CGGGGTGGTC  150
78      CGGGCTGAAG  AGCCAGGCAG  CCAAGGCAGC  CACCCCGGGG  GGTGGGCGAC  200
80      TTTGGGGGAG  TTGGTGCCCC  GCCCCCAGG  CCTTGGCGGG  GTC  ATG  246
81                                     Met
82                                     1
84      GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
85      Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
86               5                10
88      GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
89      Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
90      15                20                25
92      CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363
93      Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys
94      30                35                40
96      AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402
97      Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln
98      45                50
100     ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441
101     Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg
102     55                60                65
104     CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480
105     Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr
106     70                75
108     AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519
109     Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys
110     80                85                90
112     GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558
113     Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
114     95                100                105
116     CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597
117     Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln
118     110                115
120     GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636
121     Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser
122     120                125                130
124     CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675
125     His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr

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126          135          140
128 CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA 714
129 Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu
130 145          150          155
132 ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT 753
133 Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser
134 160          165          170
136 CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA 792
137 Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu
138 175          180
140 ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG 831
141 Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu
142 185          190          195
144 GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC 870
145 Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser
146 200          205
148 AAT GCA ACC TCC CGG GGT GCT GAA GGC CCC CTG CCC CCT 909
149 Asn Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro
150 210          215          220
152 CCC AGC ATG CCT GCA GTG GCT GGG GCA GCA GGG GGG CTG 948
153 Pro Ser Met Pro Ala Val Ala Gly Ala Ala Gly Gly Leu
154 225          230          235
156 GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC 987
157 Ala Leu Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala
158 240          245
160 ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT 1026
161 Met Cys Trp Arg Arg Arg Arg Ala Lys Pro Ser Glu Ser
162 250          255          260
164 CGC CAC CCT GGT CCT GGC TCC TTC GGG AGG GGA GGG TCT 1065
165 Arg His Pro Gly Pro Gly Ser Phe Gly Arg Gly Gly Ser
166 265          270
168 CTG GGC CTG GGG GGT GGA GGT GGG ATG GGA CCT CGG GAG 1104
169 Leu Gly Leu Gly Gly Gly Gly Gly Met Gly Pro Arg Glu
170 275          280          285
172 GCT GAG CCT GGG GAG CTA GGG ATA GCT CTG CGG GGT GGC 1143
173 Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly
174 290          295          300
176 GGG GCT GCA GAT CCC CCC TTC TGC CCC CAC TAT GAG AAG 1182
177 Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys
178 305          310
180 GTG AGT GGT GAC TAT GGG CAT CCT GTG TAT ATC GTG CAG 1221
181 Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln
182 315          320          325
184 GAT GGG CCC CCC CAG AGC CCT CCA AAC ATC TAC TAC ACA 1260
185 Asp Gly Pro Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Thr
186 330          335
188 TCG ATT TCT GTG TTG GAG TGG CCC ATA TTG CAT ACG ATA 1299
189 Ser Ile Ser Val Leu Glu Trp Pro Ile Leu His Thr Ile
190 340          345          350

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192 CAA CTG TTT TTC ATG CGA TCC AAG TGC TCC CGT GTC ACT 1338
193 Gln Leu Phe Phe Met Arg Ser Lys Cys Ser Arg Val Thr
194      355      360      365
196 ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT 1377
197 Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr
198      370      375
200 TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA 1416
201 Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro
202      380      385      390
204 TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA 1455
205 Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg
206      395      400
208 ATC AGA TGG TGT TTC TGG GGG GAC AGG ATC CTG GGT ACG 1494
209 Ile Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr
210 405      410      415
212 GCT CTG TTT GTG CTT GTG CTT ATT CTT CTT GGG AGG 1533
213 Ala Leu Phe Val Leu Val Leu Ile Leu Leu Leu Gly Arg
214 420      425      430
216 CTG AAT ATG CAT CAG ACG ACA CTG CTC CGG CAA CGG GCC 1572
217 Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala
218      435      440
220 AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610
221 Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu
222 445      450      455
224 ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660
226 GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710
228 CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CTTTCTTCCC ACAGAATTTA 1760
230 TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG TGCTGCCTGT 1810
232 CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGAATTCTGA TATCAAGCTT 1860
234 ATCGATACCG TCGACCT 1877
236 (2) INFORMATION FOR SEQ ID NO: 2:
238 (i) SEQUENCE CHARACTERISTICS:
239 (A) LENGTH: 455 amino acids
240 (B) TYPE: Amino Acid
241 (D) TOPOLOGY: Linear
243 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
245 Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala
246 1      5      10      15
248 Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu
249      20      25      30
251 Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu
252      35      40      45
254 Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu
255      50      55      60
257 Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn
258      65      70      75
260 Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg
261      80      85      90
263 Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp

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264		95		100		105
266	Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln Glu Tyr					
267		110		115		120
269	Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser His His Asp Tyr					
270		125		130		135
272	Tyr Ile Ile Ala Thr Ser Asp Gly Thr Arg Glu Gly Leu Glu Ser					
273		140		145		150
275	Leu Gln Gly Gly Val Cys Leu Thr Arg Gly Met Lys Val Leu Leu					
276		155		160		165
278	Arg Val Gly Gln Ser Pro Arg Gly Gly Ala Val Pro Arg Lys Pro					
279		170		175		180
281	Val Ser Glu Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser					
282		185		190		195
284	Leu Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser Asn					
285		200		205		210
287	Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro Pro Ser Met					
288		215		220		225
290	Pro Ala Val Ala Gly Ala Ala Gly Gly Leu Ala Leu Leu Leu Leu					
291		230		235		240
293	Gly Val Ala Gly Ala Gly Gly Ala Met Cys Trp Arg Arg Arg Arg					
294		245		250		255
296	Ala Lys Pro Ser Glu Ser Arg His Pro Gly Pro Gly Ser Phe Gly					
297		260		265		270
299	Arg Gly Gly Ser Leu Gly Leu Gly Gly Gly Gly Gly Met Gly Pro					
300		275		280		285
302	Arg Glu Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly					
303		290		295		300
305	Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys Val Ser					
306		305		310		315
308	Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln Asp Gly Pro Pro					
309		320		325		330
311	Gln Ser Pro Pro Asn Ile Tyr Tyr Thr Ser Ile Ser Val Leu Glu					
312		335		340		345
314	Trp Pro Ile Leu His Thr Ile Gln Leu Phe Phe Met Arg Ser Lys					
315		350		355		360
317	Cys Ser Arg Val Thr Thr Phe Leu Phe Pro Val Gln Val Ile Thr					
318		365		370		375
320	Thr Ser Thr Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn					
321		380		385		390
323	Pro Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg Ile					
324		395		400		405
326	Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr Ala Leu Phe					
327		410		415		420
329	Val Leu Val Leu Ile Leu Leu Leu Gly Arg Leu Asn Met His Gln					
330		425		430		435
332	Thr Thr Leu Leu Arg Gln Arg Ala Ser Val Glu Ala Glu Ala Gly					
333		440		445		450
335	Gln His Gly Pro Leu					
336		455				

VERIFICATION SUMMARY

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Output Set: N:\CRF3\02012002\J021121.raw

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]